

lactoferrin is substantially identical to native human milk lactoferrin in terms of molecular mass and recognition by anti-lactoferrin antibody.

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(iii) NUMBER OF SEQUENCES: 8

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2086 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..2086

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GGA TCC GGC CGT AGG AGA AGG AGT GTT CAG TGG TGC GCC GTA TCC CAA	48
Gly Ser Gly Arg Arg Arg Ser Val Gln Trp Cys Ala Val Ser Gln	
1 5 10 15	
CCC GAG GCC ACA AAA TGC TTC CAA TGG CAA AGG AAT ATG AGA AAA GTG	96
Pro Glu Ala Thr Lys Cys Phe Gln Trp Gln Arg Asn Met Arg Lys Val	
20 25 30	
CGT GGC CCT CCT GTC AGC TGC ATA AAG AGA GAC TCC CCC ATC CAG TGT	144
Arg Gly Pro Pro Val Ser Cys Ile Lys Arg Asp Ser Pro Ile Gln Cys	
35 40 45	
ATC CAG GCC ATT GCG GAA AAC AGG GCC GAT GCT GTG ACC CTT GAT GGT	192
Ile Gln Ala Ile Ala Glu Asn Arg Ala Asp Ala Val Thr Leu Asp Gly	
50 55 60	
GGT TTC ATA TAC GAG GCA GGC CTG GCC CCC TAC AAA CTG CGA CCT GTA	240
Gly Phe Ile Tyr Glu Ala Gly Leu Ala Pro Tyr Lys Leu Arg Pro Val	
65 70 75 80	
GCG GCG GAA GTC TAC GGG ACC GAA AGA CAG CCA CGA ACT CAC TAT TAT	288
Ala Ala Glu Val Tyr Gly Thr Glu Arg Gln Pro Arg Thr His Tyr Tyr	
85 90 95	
GCC GTG GCT GTG GTG AAG AAG GGC GGC AGC TTT CAG CTG AAC GAA CTG	336
Ala Val Ala Val Val Lys Lys Gly Gly Ser Phe Gln Leu Asn Glu Leu	
100 105 110	
CAA GGT CTG AAG TCC TGC CAC ACA GGC CTT CGC AGG ACC GCT GGA TGG	384
Gln Gly Leu Lys Ser Cys His Thr Gly Leu Arg Arg Thr Ala Gly Trp	

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115	120	125	
AAT GTC CCT ATA GGG ACA CTT CGT CCA TTC TTG AAT TGG ACG GGT CCA Asn Val Pro Ile Gly Thr Leu Arg Pro Phe Leu Asn Trp Thr Gly Pro 130 135 140			432
CCT GAG CCC ATT GAG GCA GCT GTG GCC AGG TTC TTC TCA GCC AGC TGT Pro Glu Pro Ile Glu Ala Ala Val Ala Arg Phe Phe Ser Ala Ser Cys 145 150 155 160			480
GTT CCC GGT GCA GAT AAA GGA CAG TTC CCC AAC CTG TGT CGC CTG TGT Val Pro Gly Ala Asp Lys Gly Gln Phe Pro Asn Leu Cys Arg Leu Cys 165 170 175			528
GCG GGG ACA GGG GAA AAC AAA TGT GCC TTC TCC TCC CAG GAA CCG TAC Ala Gly Thr Gly Glu Asn Lys Cys Ala Phe Ser Ser Gln Glu Pro Tyr 180 185 190			576
TTC AGC TAC TCT GGT GCC TTC AAG TGT CTG AGA GAC GGG GCT GGA GAC Phe Ser Tyr Ser Gly Ala Phe Lys Cys Leu Arg Asp Gly Ala Gly Asp 195 200 205			624
GTG GCT TTT ATC AGA GAG AGC ACA GTG TTT GAG GAC CTG TCA GAC GAG Val Ala Phe Ile Arg Glu Ser Thr Val Phe Glu Asp Leu Ser Asp Glu 210 215 220			672
GCT GAA AGG GAC GAG TAT GAG TTA CTC TGC CCA GAC AAC ACT CGG AAG Ala Glu Arg Asp Glu Tyr Glu Leu Leu Cys Pro Asp Asn Thr Arg Lys 225 230 235 240			720
CCA GTG GAC AAG TTC AAA GAC TGC CAT CTG GCC CGG GTC CCT TCT CAT Pro Val Asp Lys Phe Lys Asp Cys His Leu Ala Arg Val Pro Ser His 245 250 255			768
GCC GTT GTG GCA CGA AGT GTG AAT GGC AAG GAG GAT GCC ATC TGG AAT Ala Val Val Ala Arg Ser Val Asn Gly Lys Glu Asp Ala Ile Trp Asn 260 265 270			816
CTT CTC CGC CAG GCA CAG GAA AAG TTT GGA AAG GAC AAG TCA CCG AAA Leu Leu Arg Gln Ala Gln Glu Lys Phe Gly Lys Asp Lys Ser Pro Lys 275 280 285			864
TTC CAG CTC TTT GGC TCC CCT AGT GGG CAG AAA GAT CTG CTG TTC AAG Phe Gln Leu Phe Gly Ser Pro Ser Gly Gln Lys Asp Leu Leu Phe Lys 290 295 300			912
GAC TCT GCC ATT GGG TTT TCG AGG GTG CCC CCG AGG ATA GAT TCT GGG Asp Ser Ala Ile Gly Phe Ser Arg Val Pro Pro Arg Ile Asp Ser Gly 305 310 315 320			960
CTG TAC CTT GGC TCC GGC TAC TTC ACT GCC ATC CAG AAC TTG AGG AAA Leu Tyr Leu Gly Ser Gly Tyr Phe Thr Ala Ile Gln Asn Leu Arg Lys 325 330 335			1008
AGT GAG GAG GAA GTG GCT GCC CGG CGT GCG CGG GTC GTG TGG TGT GCG Ser Glu Glu Glu Val Ala Ala Arg Arg Ala Arg Val Val Trp Cys Ala 340 345 350			1056
GTG GGC GAG CAG GAG CTG CGC AAG TGT AAC CAG TGG AGT GGC TTG AGC Val Gly Glu Gln Glu Leu Arg Lys Cys Asn Gln Trp Ser Gly Leu Ser 355 360 365			1104
GAA GGC AGC GTG ACC TGC TCC TCG GCC TCC ACC ACA GAG GAC TGC ATC Glu Gly Ser Val Thr Cys Ser Ser Ala Ser Thr Thr Glu Asp Cys Ile 370 375 380			1152
GCC CTG GTG CTG AAA GGA GAA GCT GAT GCC ATG AGT TTG GAT GGA GGA Ala Leu Val Leu Lys Gly Glu Ala Asp Ala Met Ser Leu Asp Gly Gly 385 390 395 400			1200
TAT GTG TAC ACT GCA GGC AAA TGT GGT TTG GTG CCT GTC CTG GCA GAG Tyr Val Tyr Thr Ala Gly Lys Cys Gly Leu Val Pro Val Leu Ala Glu 405 410 415			1248
AAC TAC AAA TCC CAA CAA AGC AGT GAC CCT GAT CCT AAC TGT GTG GAT Asn Tyr Lys Ser Gln Gln Ser Ser Asp Pro Asp Pro Asn Cys Val Asp 420 425 430			1296
AGA CCT GTG GAA GGA TAT CTT GCT GTG GCG GTG GTT AGG AGA TCA GAC			1344

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Arg	Pro	Val	Glu	Gly	Tyr	Leu	Ala	Val	Ala	Val	Val	Arg	Arg	Ser	Asp		
		435						440					445				
ACT	AGC	CTT	ACC	TGG	AAC	TCT	GTG	AAA	GGC	AAG	AAG	TCC	TGC	CAC	ACC	1392	
Thr	Ser	Leu	Thr	Trp	Asn	Ser	Val	Lys	Gly	Lys	Lys	Ser	Cys	His	Thr		
		450				455					460						
GCC	GTG	GAC	AGG	ACT	GCA	GGC	TGG	AAT	ATC	CCC	ATG	GGC	CTG	CTC	TTC	1440	
Ala	Val	Asp	Arg	Thr	Ala	Gly	Trp	Asn	Ile	Pro	Met	Gly	Leu	Leu	Phe		
		465				470				475					480		
AAC	CAG	ACG	GGC	TCC	TGC	AAA	TTT	GAT	GAA	TAT	TTC	AGT	CAA	AGC	TGT	1488	
Asn	Gln	Thr	Gly	Ser	Cys	Lys	Phe	Asp	Glu	Tyr	Phe	Ser	Gln	Ser	Cys		
				485					490					495			
GCC	CCT	GGG	TCT	GAC	CCG	AGA	TCT	AAT	CTC	TGT	GCT	CTG	TGT	ATT	GGC	1536	
Ala	Pro	Gly	Ser	Asp	Pro	Arg	Ser	Asn	Leu	Cys	Ala	Leu	Cys	Ile	Gly		
				500				505					510				
GAC	GAG	CAG	GGT	GAG	AAT	AAG	TGC	GTG	CCC	AAC	AGC	AAC	GAG	AGA	TAC	1584	
Asp	Glu	Gln	Gly	Glu	Asn	Lys	Cys	Val	Pro	Asn	Ser	Asn	Glu	Arg	Tyr		
				515			520					525					
TAC	GGC	TAC	ACT	GGG	GCT	TTC	CGG	TGC	CTG	GCT	GAG	AAT	GCT	GGA	GAC	1632	
Tyr	Gly	Tyr	Thr	Gly	Ala	Phe	Arg	Cys	Leu	Ala	Glu	Asn	Ala	Gly	Asp		
						535					540						
GTT	GCA	TTT	GTG	AAA	GAT	GTC	ACT	GTC	TTG	CAG	AAC	ACT	GAT	GGA	AAT	1680	
Val	Ala	Phe	Val	Lys	Asp	Val	Thr	Val	Leu	Gln	Asn	Thr	Asp	Gly	Asn		
						550				555					560		
AAC	AAT	GAG	GCA	TGG	GCT	AAG	GAT	TTG	AAG	CTG	GCA	GAC	TTT	CGG	CTG	1728	
Asn	Asn	Glu	Ala	Trp	Ala	Lys	Asp	Leu	Lys	Leu	Ala	Asp	Phe	Ala	Leu		
						565			570					575			
CTG	TGC	CTC	GAT	GGC	AAA	CGG	AAG	CCT	GTG	ACT	GAG	GCT	AGA	AGC	TGC	1776	
Leu	Cys	Leu	Asp	Gly	Lys	Arg	Lys	Pro	Val	Thr	Glu	Ala	Arg	Ser	Cys		
						580		585					590				
CAT	CTT	GCC	ATG	GCC	CCG	AAT	CAT	GCC	GTG	GTG	TCT	CGG	ATG	GAT	AAG	1824	
His	Leu	Ala	Met	Ala	Pro	Asn	His	Ala	Val	Val	Ser	Arg	Met	Asp	Lys		
						595		600					605				
GTG	GAA	CGC	CTG	AAA	CAG	GTG	TTG	CTC	CAC	CAA	CAG	GCT	AAA	TTT	GGG	1872	
Val	Glu	Arg	Leu	Lys	Gln	Val	Leu	Leu	His	Gln	Gln	Ala	Lys	Phe	Gly		
						610		615				620					
AGA	AAT	GGA	TCT	GAC	TGC	CCG	GAC	AAG	TTT	TGC	TTA	TTC	CAG	TCT	GAA	1920	
Arg	Asn	Gly	Ser	Asp	Cys	Pro	Asp	Lys	Phe	Cys	Leu	Phe	Gln	Ser	Glu		
						625		630		635					640		
ACC	AAA	AAC	CTT	CTG	TTC	AAT	GAC	AAC	ACT	GAG	TGT	CTG	GCC	AGA	CTC	1968	
Thr	Lys	Asn	Leu	Leu	Phe	Asn	Asp	Asn	Thr	Glu	Cys	Leu	Ala	Arg	Leu		
						645			650				655				
CAT	GGC	AAA	ACA	ACA	TAT	GAA	AAA	TAT	TTG	GGA	CCA	CAG	TAT	GTC	GCA	2016	
His	Gly	Lys	Thr	Thr	Tyr	Glu	Lys	Tyr	Leu	Gly	Pro	Gln	Tyr	Val	Ala		
						660		665					670				
GGC	ATT	ACT	AAT	CTG	AAA	AAG	TGC	TCA	ACC	TCC	CCC	CTC	CTG	GAA	GCC	2064	
Gly	Ile	Thr	Asn	Leu	Lys	Lys	Cys	Ser	Thr	Ser	Pro	Leu	Leu	Glu	Ala		
						675		680				685					
TGT	GAA	TTC	CTC	AGG	AAG	TAA	A									2086	
Cys	Glu	Phe	Leu	Arg	Lys	*											
						690		695									

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 694 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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Gly	Ser	Gly	Arg	Arg	Arg	Ser	Val	Gln	Trp	Cys	Ala	Val	Ser	Gln	
1				5				10					15		
Pro	Glu	Ala	Thr	Lys	Cys	Phe	Gln	Trp	Gln	Arg	Asn	Met	Arg	Lys	Val
			20					25					30		
Arg	Gly	Pro	Pro	Val	Ser	Cys	Ile	Lys	Arg	Asp	Ser	Pro	Ile	Gln	Cys
		35					40					45			
Ile	Gln	Ala	Ile	Ala	Glu	Asn	Arg	Ala	Asp	Ala	Val	Thr	Leu	Asp	Gly
	50					55					60				
Gly	Phe	Ile	Tyr	Glu	Ala	Gly	Leu	Ala	Pro	Tyr	Lys	Leu	Arg	Pro	Val
	65			70					75					80	
Ala	Ala	Glu	Val	Tyr	Gly	Thr	Glu	Arg	Gln	Pro	Arg	Thr	His	Tyr	Tyr
			85						90					95	
Ala	Val	Ala	Val	Val	Lys	Lys	Gly	Gly	Ser	Phe	Gln	Leu	Asn	Glu	Leu
			100					105					110		
Gln	Gly	Leu	Lys	Ser	Cys	His	Thr	Gly	Leu	Arg	Arg	Thr	Ala	Gly	Trp
		115					120					125			
Asn	Val	Pro	Ile	Gly	Thr	Leu	Arg	Pro	Phe	Leu	Asn	Trp	Thr	Gly	Pro
	130					135					140				
Pro	Glu	Pro	Ile	Glu	Ala	Ala	Val	Ala	Arg	Phe	Phe	Ser	Ala	Ser	Cys
	145				150				155					160	
Val	Pro	Gly	Ala	Asp	Lys	Gly	Gln	Phe	Pro	Asn	Leu	Cys	Arg	Leu	Cys
			165					170					175		
Ala	Gly	Thr	Gly	Glu	Asn	Lys	Cys	Ala	Phe	Ser	Ser	Gln	Glu	Pro	Tyr
		180						185					190		
Phe	Ser	Tyr	Ser	Gly	Ala	Phe	Lys	Cys	Leu	Arg	Asp	Gly	Ala	Gly	Asp
		195					200					205			
Val	Ala	Phe	Ile	Arg	Glu	Ser	Thr	Val	Phe	Glu	Asp	Leu	Ser	Asp	Glu
		210				215					220				
Ala	Glu	Arg	Asp	Glu	Tyr	Glu	Leu	Leu	Cys	Pro	Asp	Asn	Thr	Arg	Lys
	225				230					235				240	
Pro	Val	Asp	Lys	Phe	Lys	Asp	Cys	His	Leu	Ala	Arg	Val	Pro	Ser	His
			245					250					255		
Ala	Val	Val	Ala	Arg	Ser	Val	Asn	Gly	Lys	Glu	Asp	Ala	Ile	Trp	Asn
		260						265					270		
Leu	Leu	Arg	Gln	Ala	Gln	Glu	Lys	Phe	Gly	Lys	Asp	Lys	Ser	Pro	Lys
		275					280					285			
Phe	Gln	Leu	Phe	Gly	Ser	Pro	Ser	Gly	Gln	Lys	Asp	Leu	Leu	Phe	Lys
	290					295					300				
Asp	Ser	Ala	Ile	Gly	Phe	Ser	Arg	Val	Pro	Pro	Arg	Ile	Asp	Ser	Gly
	305				310				315					320	
Leu	Tyr	Leu	Gly	Ser	Gly	Tyr	Phe	Thr	Ala	Ile	Gln	Asn	Leu	Arg	Lys
			325					330					335		
Ser	Glu	Glu	Glu	Val	Ala	Ala	Arg	Arg	Ala	Arg	Val	Val	Trp	Cys	Ala
			340					345					350		
Val	Gly	Glu	Gln	Glu	Leu	Arg	Lys	Cys	Asn	Gln	Trp	Ser	Gly	Leu	Ser
		355					360					365			
Glu	Gly	Ser	Val	Thr	Cys	Ser	Ser	Ala	Ser	Thr	Thr	Glu	Asp	Cys	Ile
	370					375						380			
Ala	Leu	Val	Leu	Lys	Gly	Glu	Ala	Asp	Ala	Met	Ser	Leu	Asp	Gly	Gly
	385				390				395					400	
Tyr	Val	Tyr	Thr	Ala	Gly	Lys	Cys	Gly	Leu	Val	Pro	Val	Leu	Ala	Glu
			405					410					415		
Asn	Tyr	Lys	Ser	Gln	Gln	Ser	Ser	Asp	Pro	Asp	Pro	Asn	Cys	Val	Asp

420	425	430
Arg Pro Val Glu Gly Tyr Leu Ala Val Ala Val Val Arg Arg Ser Asp 435	440	445
Thr Ser Leu Thr Trp Asn Ser Val Lys Gly Lys Lys Ser Cys His Thr 450	455	460
Ala Val Asp Arg Thr Ala Gly Trp Asn Ile Pro Met Gly Leu Leu Phe 465	470	475
Asn Gln Thr Gly Ser Cys Lys Phe Asp Glu Tyr Phe Ser Gln Ser Cys 485	490	495
Ala Pro Gly Ser Asp Pro Arg Ser Asn Leu Cys Ala Leu Cys Ile Gly 500	505	510
Asp Glu Gln Gly Glu Asn Lys Cys Val Pro Asn Ser Asn Glu Arg Tyr 515	520	525
Tyr Gly Tyr Thr Gly Ala Phe Arg Cys Leu Ala Glu Asn Ala Gly Asp 530	535	540
Val Ala Phe Val Lys Asp Val Thr Val Leu Gln Asn Thr Asp Gly Asn 545	550	555
Asn Asn Glu Ala Trp Ala Lys Asp Leu Lys Leu Ala Asp Phe Ala Leu 565	570	575
Leu Cys Leu Asp Gly Lys Arg Lys Pro Val Thr Glu Ala Arg Ser Cys 580	585	590
His Leu Ala Met Ala Pro Asn His Ala Val Val Ser Arg Met Asp Lys 595	600	605
Val Glu Arg Leu Lys Gln Val Leu Leu His Gln Gln Ala Lys Phe Gly 610	615	620
Arg Asn Gly Ser Asp Cys Pro Asp Lys Phe Cys Leu Phe Gln Ser Glu 625	630	635
Thr Lys Asn Leu Leu Phe Asn Asp Asn Thr Glu Cys Leu Ala Arg Leu 645	650	655
His Gly Lys Thr Thr Tyr Glu Lys Tyr Leu Gly Pro Gln Tyr Val Ala 660	665	670
Gly Ile Thr Asn Leu Lys Lys Cys Ser Thr Ser Pro Leu Leu Glu Ala 675	680	685
Cys Glu Phe Leu Arg Lys 690	695	

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

AGCGGATCCG GCCGTAGGAG AAGGAGTGTT CAGTGG

36

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CGATCTAGAT TACTTCCTGA GGAATCCACA GGC 33

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 42 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

AAGCTTATGA AACTGTCTT CCTCGTCTG TTCTTCCTCG GG 42

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 35 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GATCCAGCCA GAGAGAGTCC GAGGGCCCG AGGAA 35

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 28 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

ATTATTCGAA ACGAGGAATT AGCTTATG 28

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

-continued

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

TCGAGAAAAG ACTTTCTCC GG

22

TCGAGAAAAG ACTTTCTCC GG